

Alpha Virus nsp4 alignment

CLUSTAL W (1.82) multiple sequence alignment

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SFV_nsp4      -----YIFSSDTGSGHLQOKSVRQHNLCQAQLDAVQEEKMYPPKLDTEREKL L L L L K M Q M   54
RRV_nsp4      -----YIFSSDTGPGHLQOKSVRQHAPCEMLYAHEEERTYPPALDEAREK L L Q A K M Q M   54
ONV_nsp4      -----YIFSSDTGQGH L Q O K S V R Q T T L P V N I V E E V H E E K C Y P P K L D E I K E Q L L L K R L Q E   54
SinV_nsp4     LTGVGGYIFSTDTGPGHLQKKSVLQNQLTEPTLERNVLERIHAPVLDT S K E E Q L K L R Y Q M   60
VEEV_nsp4     -----YIFSSDTGQGH L Q O K S V R Q T V L S E V V L E R T E L E I S Y A P R L D Q E K E E L L R K K L Q L   54
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SFV_nsp4      HPSEANKSRYSQSRKVENMKATVVDRLTSGARLYTGADVGRIPYAVRYPRPVYSPTVIER 114
RRV_nsp4      APTEANKSRYSQSRKVENMKAVIIDRLKDGARTYLAEQSEKIPTYASKYPRPVYSPSVEDS 114
ONV_nsp4      SASTANRSRYQSRKVENMKATIIHRLKEGCRLLYLASETPRVPSYRVITYPAPIYSPSINIK 114
SinV_nsp4     MPTEANKSRYSQSRKVENQKAITTERLLSGLRLYNS-ATDQPECYKITYPKPLYSSSV PAN 119
VEEV_nsp4     NPTPANRSRYQSRKVENMKAITARRILQGLGHY L K-AEGKVECYRTLHPVPLYSSSVNRA 113
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SFV_nsp4      FSSPDVAIAACNEYLSRNYPTVASYQITDEYDAYLDMVDGSDSCLDRATFCPAKLR CY PK 174
RRV_nsp4      LQSPEVAVAAACNAFLEANYPTVASYQITDEYDAYLDMVDGSESC L DRATFCPAKLR CY PK 174
ONV_nsp4      LTNPETAVAVCN EFLARNYPTVASYQVTDEYDAYLDMVDGSESC L DRATFNPSKLRSY PK 174
SinV_nsp4     YSDPQFAVAVCN NYLHENYPTVASYQITDEYDAYLDMVDGTVACLD TATFCPAKLRSY PK 179
VEEV_nsp4     FSSPKVAVEACNAMLKENFPTVASYCI IPEYDAYLDMVDGASCC LDTASFCPAKLRSFPK 173
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SFV_nsp4      HHAYHQPTVRSVAVPSPFQNTLQNVLAAATKRNCNVTQMRELPTMDSAVFNVECFKRYACS 234
RRV_nsp4      HHAYHQPVRSVAVPSPFQNTLQNVLAAATKRNCNVTQMRELPTLDSAVFNVECFKKFACN 234
ONV_nsp4      QHSYHAPTIRSAVPSPFQNTLQNVLAAATKRNCNVTQMRELPTMDSAVFNVECFKKYACN 234
SinV_nsp4     KHEYRAPNIRSAVPSAMQNTLQNVLIAATKRNCNVTQMRELPTLDSATFNVECFRKYACN 239
VEEV_nsp4     KHSYLEPTIRSAVPSAIQNTLQNVLAAATKRNCNVTQMREL PVLDSAAFNVECFKKYACN 233
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SFV_nsp4      GEYWEEYAKQPIRITTENITTYVTKLKGPKAAALFAKTHNLVPLQEVPMDRFTVDMKR DV 294
RRV_nsp4      GEYWQEFKDDPIRITTENITTYVTRLKGPKAAALFAKTHNLVPLQEVPMDRFVDMKR DV 294
ONV_nsp4      QEYWREFASSPIRVTTENLTMYVTKLKGPKAAALFAKTHNLLPLQEVPMDRFTMDMKR DV 294
SinV_nsp4     DEYWEEFARKPIRITTEFVTAYVARLKGPKAAALFAKTYNLVPLQEVPMDRFVDMKR DV 299
VEEV_nsp4     NEYWETFKENPIRLTEENVVNYITKLKGPKAAALFAKTHNLNMLQDIPMDRFVMDLKR DV 293
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SFV_nsp4      KVTGPGTKHTEERPKVQVQIAAEPLATAYLCGIHRELVRRLNAVL RPNVHTLFDM SAE DFD 354
RRV_nsp4      KVTGPGTKHTEERPKVQVQIAAEPLATAYLCGIHRELVRRLKAVLAPNIHTLFDM SAE DFD 354
ONV_nsp4      KVTGPGTKHTEERPKVQVQIAAEPLATAYLCGIHRELVRRLNAVL L PNVHTLFDM SAE DFD 354
SinV_nsp4     KVTGPGTKHTEERPKVQVQIAAEPLATAYLCGIHRELVRRLTAVLLPNIHTLFDM SAE DFD 359
VEEV_nsp4     KVTGPGTKHTEERPKVQVQIAADPLATADLCGIHRELVRRLNAVL L PNIHTLFDM SAE DFD 353
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SFV_nsp4      AIIASHFHGDPVLETDIASFDKSQDDSLALTGLMILEDLGVDQYLLDLIEAAFGEISSC 414
RRV_nsp4      AIIAAHFQPGDAVLETDIASFDKSQDDSLALTALMLLEDLGVDQELLDLIEAAFGEITSV 414
ONV_nsp4      AIIATHFKPGDAVLETDIASFDKSQDDSLASTAMMLLEDLGVDQPILDLIEAAFGEISSC 414
SinV_nsp4     AIIAEHFQKQGDPVLETDIASFDKSQDDAMALTGLMILEDLGVDQPLLDLIECAFGEISST 419
VEEV_nsp4     AIIAEHFQPGDCVLETDIASFDKSEDDAMALTALMILEDLGVD AELLTLIEAAFGEISSI 413
               *****: ** *****:***: * *:*****: * *** *****:

SFV_nsp4      HLPTGTRFKFGAMMKSGMFLTLFINTVLNITIASRVLEQRLTDSACAAFIGDDNIVHGVI 474
RRV_nsp4      HLPTGTRFKFGAMMKSGMFLTLFINTLLNIVIA CRVLREKLTNSICAAFIGDDNIVHGVR 474
ONV_nsp4      HLPTGTRFKFGAMMKSGMFLTLFVNTLLNITIASRVLEERLTTSACAAFIGDDNIIHG VV 474
SinV_nsp4     HLPTGTRFKFGAMMKSGMFLTLFVNTVLNVVIASRVLEERLKT SRCAAFIGDDNIIHG VV 479
VEEV_nsp4     HLPTKTKFKFGAMMKSGMFLTLFVNTVINIVIASRVLRERLTGSPCAAFIGDDNIVKG V K 473
               *****:*****:***:*. *.***:*. * *****:***

SFV_nsp4      SDKLMAERCASWVNMEVKIIDAVMGEKPPYFCGGFIVFDSVTQTACRVSDPLKRLFKLGK 534
RRV_nsp4      SDPLMAERCASWVNMEVKIIDATMCEKPPYFCGGFIFYDNVTGSACRVADPLKRLFKLGK 534
ONV_nsp4      SDALMAARCATWMNMEVKIIDAVVSEKAPYFCGGFILHDTVTGTSCR VADPLKRLFKLGK 534
SinV_nsp4     SDKEMAERCATWLNMEVKIIDAVIGERPPYFCGGFILQDSVTSTACRVADPLKRLFKLGK 539
VEEV_nsp4     SDKLMADRCATWLNMEVKIIDAVVGEKAPYFCGGFILCDSVTGTACRVADPLKRLFKLGK 533
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SFV_nsp4	PLTAEDKQDEDRRRALSDEVSKWERTGLGAELEVALTSRYEVEGCKSILIAMTTLARDIK	594
RRV_nsp4	PLPAGDTQDEDRRRALKDETDRWARVGLKSELEIALSSRYEVNGTGNIVRAMATLAKSLK	594
ONV_nsp4	PLAAGDEQDEDRRRALADEVTRWQRTGLVTELEKAVYSRYEVQGITAVITSMATFANSKE	594
SinV_nsp4	PLPADDEQDEDRRRALLDETKAWFRVGITGTLAVAVTTRYEVDNITPVLLALRTFAQSKR	599
VEEV_nsp4	PLAVDDEHDDDRRRALHEESTRWNRVGILPELCKAVESRYETVGTSSIIVMAMTTLASSVK	593
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SFV_nsp4	AFKKLRGPVIHLYGGPRLVR	614
RRV_nsp4	NFKKLRGPIVHLYGGPK---	611
ONV_nsp4	NFKKLRGPVVTLYGGPK---	611
SinV_nsp4	AFQAIRGEIKHLYGGPK---	616
VEEV_nsp4	SFSYLRGAPITLY-----	606
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